



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/678,588
Source: IFW9
Date Processed by STIC: 5/26/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202



IFWO

RAW SEQUENCE LISTING

DATE: 05/26/2004

PATENT APPLICATION: US/10/678,588

TIME: 15:38:44

Input Set : D:\52578C.ST25.txt

Output Set: N:\CRF4\05262004\J678588.raw

3 <110> APPLICANT: Jingrui Wu
 5 <120> TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants
 7 <130> FILE REFERENCE: 38-15(52578)C
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/678,588
 C--> 9 <141> CURRENT FILING DATE: 2003-10-02
 9 <160> NUMBER OF SEQ ID NOS: 10
 11 <170> SOFTWARE: PatentIn version 3.2
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2480
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Artificial
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: transcriptional unit comprising promoter, coding sequence for
 20 transcription factor of SEQ ID NO:2 and terminator elements
 22 <400> SEQUENCE: 1
 23 aggatattaa agtatgtatt catcattaat ataatcagtg tattccaata tgtactacga 60
 25 tttccaatgt ctttattgtc gccgtatgta atcggcgtca caaaataatc cccggtgact 120
 27 ttcttttaat ccaggatgaa ataatatgtt attataattt ttgcgatttg gtccgttata 180
 29 ggaattgaag tgtgcttgag ctccggtcgcc accactccca ttccataatt ttacatgtat 240
 31 ttgaaaaata aaaatttatg gtattcaatt taaacacgta tacttgtaaa gaatgatatc 300
 33 ttgaaagaaa tatagtttaa atattttattg ataaaaataac aagtcaggta ttatagtcca 360
 35 agcaaaaaca taaatttatt gatgcaagtt taaattcaga aatatttcaa taactgatta 420
 37 tatcagctgg tacattgccg tagatgaaag actgagtgcg atattatgtg taatacataa 480
 39 attgatgata tagctagaac tagtggatcc cccgggccct gcaggctcga gctagtttga 540
 41 gatatccccg ttatggtact ggggttgcat ataaccatt ccttggttgt atgctccctg 600
 43 ttggcccatc ccttggtgcag ctgagctact tgctccaca tgaccaaggg catccttttt 660
 45 aattgagcca tcgctagatt ttgcagttaa cttgctatca cctccatct ctctgtactt 720
 47 ctgcaggtac accttgaggg gttcaatgta gtcttcaaac cccagcgtgg ccatggccca 780
 49 cagcagatcg tcgccattga tgggtcttcg cttctccctc tggcacttgt cactcgcttc 840
 51 gctagtgatg aaggagatga actcggagac gcactcctgc acggtctcct tagcgtcctt 900
 53 ggcgatcttc ccgttagccg ggatggctct cccgttagcc gggatggcct tcttcatgat 960
 55 gcgactgatg ttggcgatgg gcaggaacct gtctgtctcc ctgacgtgc caccgcctcc 1020
 57 gcctcccctg gggctcccgc tctcgtgget cccgccgccg ccgccagggc tcgccggagc 1080
 59 ttccgccatg gtctacctac aaaaaagctc cgcacgagggc tgcatttgct acaaatcatg 1140
 61 aaaagaaaaa ctaccgatga acaatgctga gggattcaaa ttctaccac aaaaagaaga 1200
 63 aagaaagatc tagcacatct aagcctgacg aagcagcaga aatatataaa aatataaacc 1260
 65 atagtgcctt tttcccctct tctgatctt gtttagcatg gcggaaattt taaaccccc 1320
 67 atcatctccc ccaacaacgg cggatcgcat atctacatcc gagagcccca ttccccgcga 1380
 69 gatccggggc ggatccacgc cggcgagagc cccagccgcg agatcccgcc cctcccgcgc 1440
 71 accgatctgg gcgcgcacga agccgcctct cgcccaccca aactaccaag gccaaagatc 1500
 73 gagaccgaga cggaaaaaaa aaacggagaa agaaagagga gaggggcggg gtggttaccg 1560
 75 gcggcgccgg aggggggaggg gggaggagct gtcgtccgg cagcgagggg ggaggaggtg 1620
 77 gtggtggtgg tgggtgtagg gttgggggga tgggaggaga ggggggggta tgtatatagt 1680

Does Not Comply
Corrected Diskette Needed

(pg. 5-9)

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Input Set : D:\52578C.ST25.txt

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```

79 ggcgatgggg ggcgtttctt tggaagcggg gggaggggccc gcctcgtcgc tggctcgcga 1740
81 tcctcctcgc gtttccggcc cccacgaccc ggaccacact gctgtttttt ctttttcttt 1800
83 tttttctttc tttttttttt tttggctgcg agacgtgcgg tgcgtgcgga caactcacgg 1860
85 tgatagtggg ggggtgtgga gactattgtc cagttggctg gactggggtg gggtgggttg 1920
87 gggtgggttg ggctgggctt gctatggatc gtggatagca ctttgggctt taggacttta 1980
89 ggggttggtt ttgtaaatgt tttgagtcta agtttatctt ttatttttac tagaaaaaat 2040
91 acccatgcgc tgcaacgggg gaaagctatt ttaatcttat tattgttcat tgtgagaatt 2100
93 cgcctgaata tatatttttc tcaaaaatta tgtcaaatta gcatatgggt ttttttaaag 2160
95 atatttctta tacaaatccc tctgtattta caaaagcaaa cgaacttaaa acccgactca 2220
97 aatacagata tgcatttcca aaagcgaata aacttaaaaa ccaattcata caaaaatgac 2280
99 gtatcaaagt accgacaaaa acatcctcaa tttttataat agtagaaaag agtaaatttc 2340
101 actttgggcc accttttatt accgatattt tactttatac caccttttaa ctgatgtttt 2400
103 cacttttgac caggtaatct tacctttggt ttattttgga ctatcccgac tctcttctca 2460
105 agcatatgaa tgacctcgag 2480
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 185
110 <212> TYPE: PRT
111 <213> ORGANISM: Zea mays
113 <400> SEQUENCE: 2
115 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu
116 1 5 10 15
119 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
120 20 25 30
123 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
124 35 40 45
127 Ile Pro Ala Asn Gly Lys Thr Ile Pro Ala Asn Gly Lys Ile Ala Lys
128 50 55 60
131 Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
132 65 70 75 80
135 Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
136 85 90 95
139 Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
140 100 105 110
143 Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
144 115 120 125
147 Glu Gly Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys
148 130 135 140
151 Lys Asp Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Gln Gly
152 145 150 155 160
155 Met Gly Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
156 165 170 175
159 Gln Tyr His Asn Gly Asp Ile Ser Asn
160 180 185
163 <210> SEQ ID NO: 3
164 <211> LENGTH: 178
165 <212> TYPE: PRT
166 <213> ORGANISM: Zea mays
168 <400> SEQUENCE: 3
170 Met Ala Glu Ala Pro Ala Ser Pro Gly Gly Gly Gly Gly Ser His Glu

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```

171 1          5          10          15
174 Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
175          20          25          30
178 Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala
179          35          40          45
182 Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln
183          50          55          60
186 Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp
187 65          70          75          80
190 Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu
191          85          90          95
194 Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys
195          100          105          110
198 Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr
199          115          120          125
202 Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val
203          130          135          140
206 Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly Gln Gln Gly Ala Tyr
207 145          150          155          160
210 Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile
211          165          170          175
214 Ser Asn
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 537
220 <212> TYPE: DNA
221 <213> ORGANISM: Zea mays
223 <400> SEQUENCE: 4
224 atggcggaag ctccggcgag ccctggcggc ggcggcgagg gccacgagag cgggagcccc 60
226 aggggaggcg gaggcggtgg cagcgtcagg gagcaggaca ggttcctgcc catcgccaac 120
228 atcagtcgca tcatgaagaa ggccatcccc gctaaccggga agatcgccaa ggacgctaag 180
230 gagaccgtgc aggagtgcgt ctccgagttc atctccttca tctactgcga agcgagtgc 240
232 aagtgccaga gggagaagcg gaagaccatc aatggcgacg atctgctgtg ggccatggcc 300
234 acgctggggt ttgaagacta cattgaaccc ctcaagggtg acctacagaa gtacagagag 360
236 atggagggtg atagcaagtt aactgctaaa tctagcgatg gctcgattaa aaaggatgct 420
238 cttggtcatg tgggagcaag tagctcagct gcagaaggga tgggccaaca gggagcatac 480
240 aaccaaggaa tgggttatat gcaacctcag taccataacg gggatatctc aaactaa 537
243 <210> SEQ ID NO: 5
244 <211> LENGTH: 522
245 <212> TYPE: DNA
246 <213> ORGANISM: Glycine max
248 <400> SEQUENCE: 5
249 atgtcggatg cgccaccgag cccgactcat gagagtgggg gcgagcagag cccgcgcggt 60
251 tcgtcgtccg gcgcgaggga gcaggaccgg tacctcccca ttgccaacat cagccgcatt 120
253 atgaagaagg ctctgctccc caacggcaag attgcaaagg atgccaaaga caccatgcag 180
255 gaatgcgttt ctgagttcat cagcttcatt accagcgagg cgagtgcgaa atgccagaag 240
257 gagaagagaa agacaatcaa tggagacgat ttgctatggg ccatggccac tttaggattt 300
259 gaagactaca tagagccgct taagggtgtac ctggctaggt acagagaggc ggagggtgac 360
261 actaaaggat ctgctagaag tggatgatga tctgctacac cagatcaagt tggccttgca 420
263 ggtcaaaatt ctgagcttgt tcatcagggt tcgctgaact atattgggtt gcagggtgaa 480

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```

265 ccacaacatc tggttatgcc ttcaatgcaa agccatgaat ag
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 173
270 <212> TYPE: PRT
271 <213> ORGANISM: Glycine max
273 <400> SEQUENCE: 6
275 Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln
276 1 5 10 15
279 Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu
280 20 25 30
283 Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn
284 35 40 45
287 Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser
288 50 55 60
291 Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys
292 65 70 75 80
295 Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala
296 85 90 95
299 Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala
300 100 105 110
303 Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly
304 115 120 125
307 Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser
308 130 135 140
311 Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln
312 145 150 155 160
315 Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu
316 165 170
319 <210> SEQ ID NO: 7
320 <211> LENGTH: 141
321 <212> TYPE: PRT
322 <213> ORGANISM: Arabidopsis thaliana
324 <400> SEQUENCE: 7
326 Met Ala Asp Thr Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly
327 1 5 10 15
330 Gly Ser Val Arg Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser
331 20 25 30
334 Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
335 35 40 45
338 Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
339 50 55 60
342 Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
343 65 70 75 80
346 Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
347 85 90 95
350 Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
351 100 105 110
354 Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
355 115 120 125

```

RAW SEQUENCE LISTING

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```

358 Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
359      130                      135                      140
362 <210> SEQ ID NO: 8
363 <211> LENGTH: 100
364 <212> TYPE: PRT
365 <213> ORGANISM: Artificial
367 <220> FEATURE:
368 <223> OTHER INFORMATION: protein consensus sequence
371 <220> FEATURE:
372 <221> NAME/KEY: MISC_FEATURE
373 <223> OTHER INFORMATION: Xaa can be Ala or Pro
375 <220> FEATURE:
376 <221> NAME/KEY: MISC_FEATURE
377 <223> OTHER INFORMATION: Xaa can be Thr or none
379 <220> FEATURE:
380 <221> NAME/KEY: MISC_FEATURE
381 <223> OTHER INFORMATION: Xaa can be Ile or none
383 <220> FEATURE:
384 <221> NAME/KEY: MISC_FEATURE
385 <223> OTHER INFORMATION: Xaa can be Pro or none
387 <220> FEATURE:
388 <221> NAME/KEY: MISC_FEATURE
389 <223> OTHER INFORMATION: Xaa can be Ala or none
391 <220> FEATURE:
392 <221> NAME/KEY: MISC_FEATURE
393 <223> OTHER INFORMATION: Xaa can be Asn or none
395 <220> FEATURE:
396 <221> NAME/KEY: MISC_FEATURE
397 <223> OTHER INFORMATION: Xaa can be Gly or none
399 <220> FEATURE:
400 <221> NAME/KEY: MISC_FEATURE
401 <223> OTHER INFORMATION: Xaa can be Lys or none
403 <220> FEATURE:
404 <221> NAME/KEY: MISC_FEATURE
405 <223> OTHER INFORMATION: Xaa can be Glu or Asp
407 <220> FEATURE:
408 <221> NAME/KEY: MISC_FEATURE
409 <223> OTHER INFORMATION: Xaa can be Val or Met
411 <220> FEATURE:
412 <221> NAME/KEY: MISC_FEATURE
413 <223> OTHER INFORMATION: Xaa can be Asp or Glu
415 <220> FEATURE:
416 <221> NAME/KEY: MISC_FEATURE
417 <223> OTHER INFORMATION: Xaa can be Arg or Lys
419 <220> FEATURE:
420 <221> NAME/KEY: MISC_FEATURE
421 <223> OTHER INFORMATION: Xaa can be Gln or Ala
423 <220> FEATURE:
424 <221> NAME/KEY: MISC_FEATURE

```

↙ pls insert
 Numeric
 identifier
 <221> and
 state the
 locations
 for each
 of the Xaa
 locations.
 pls see
 error
 explanation
 on pg. 7

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/678,588

DATE: 05/26/2004
TIME: 15:38:45

Input Set : D:\52578C.ST25.txt
Output Set: N:\CRF4\05262004\J678588.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 22,26,27,28,29,30,31,38,40,57,61,93,94,98

Seq#:9; Xaa Pos. 29

Seq#:10; Xaa Pos. 2,3,4,6

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,8,9,10

VARIABLE LOCATION SUMMARY

DATE: 05/26/2004

PATENT APPLICATION: US/10/678,588

TIME: 15:38:45

Input Set : D:\52578C.ST25.txt

Output Set: N:\CRF4\05262004\J678588.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:8; Xaa Pos. 22,26,27,28,29,30,31,38,40,57,61,93,94,98

Seq#:9; Xaa Pos. 29

Seq#:10; Xaa Pos. 2,3,4,6

<210> SEQ ID NO 9
 <211> LENGTH: 55
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: consensus protein sequence
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Xaa can be Gln or Glu
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (29)..()
 <223> OTHER INFORMATION: Xaa can be Gln or Glu
 <400> SEQUENCE: 9
 Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp
 1 5 10 15
 Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Xaa Gly Met Gly
 20 25 30
 Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr
 35 40 45
 His Asn Gly Asp Ile Ser Asn
 50 55

delete

<210> SEQ ID NO 10
 <211> LENGTH: 8
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: consensus protein sequence
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (2)..(4)
 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 <400> SEQUENCE: 10
 Met Xaa Xaa Xaa Pro Xaa Ser Pro
 1 5

delete

← what about location 6?

pls explain ← pls see error explanation on pg. 7

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/678,588

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Input Set : D:\52578C.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:437 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:32
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:80
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0